#3

SEQUENCE LISTING

<110> Shi, Jinrui
      Beach, Larry
      Wang, Hongyu
      Rafalski, Antoni J.
      Cahoon, Rebecca E.

<120> Novel Inositol Polyphosphate Kinase
      Genes and Uses Thereof

<130> 1286

<140> US 10/042,894
<141> 2002-01-09

<150> US 60/261,465
<151> 2001-01-12

<160> 37

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<213> Zea mays

<220>
<221> CDS
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cttgctccca tagtccccat acc atg ccc gac ctc cac ccg ccg gag cac caa 113
                        Met Pro Asp Leu His Pro Pro Glu His Gln
                         1   5   10

gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc ccg ctc atc gac   161
Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
              15   20   25

ggc tcc ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag   209
Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
          30   35   40

cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg   257
His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro
      45   50   55

gcc cgc atc cga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc   305
Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
  60   65   70

ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc   353

1

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Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
 75              80              85              90

gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag   401
Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys
             95              100             105

atc ggc gcc atc acg tgg cca ccg agt tcg ccg gag ccc tac atc gcc   449
Ile Gly Ala Ile Thr Trp Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala
             110             115             120

aag tac ctc gcc aag gac cgc ggg acc acg agc gtt ctg ctc gga ttc   497
Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe
             125             130             135

cgc gtc ttg cgt ccg agt cgt cgg ccc cga ggg cgc cgt gtg gcg gac   545
Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Arg Val Ala Asp
     140             145             150

gga gcg ccc gga ggt gaa ggc tat gga cac cgt cgg cgt ccg ccg cgt   593
Gly Ala Pro Gly Gly Glu Gly Tyr Gly His Arg Arg Arg Pro Pro Arg
155             160             165             170

gct ccg gcg cta cgt gtc atc cgc ttg ccg acg agg gga tgg act gcg   641
Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala
             175             180             185

cgc tcg cgg cgg cgg tgt acg gag gaa aag gtg gag tct tgt cac agc   689
Arg Ser Arg Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser
             190             195             200

tgc gcg agc tca agg cat ggt tgg agg agc aga ctc tgt tcc act tct   737
Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser
             205             210             215

act cgg cgt cga ttc ttc tgg gct atg atg ctg ctg cag tcg cag cag   785
Thr Arg Arg Arg Phe Phe Trp Ala Met Met Leu Leu Gln Ser Gln Gln
             220             225             230

gcg gag gtg ggg gtg ggg taa cagtgaagct ggtggacttt gcccatgtgg      836
Ala Glu Val Gly Val Gly  *
235             240

ccgagggtga tggggtgatt gaccacaact tcctgggcga gctctgctag ctgatcaagt  896
tcgtttctga cattgttcca gagactcctt agacgcagcc tttgggtcct tcttaagaga  956
ggatcctgac atttttgatt tgataacaaa ggaagcactt tcagctgcaa aaaaagaaag 1016
cagcagtgag gatgaagatg acagtagtga ggaaagttcg gatgatgagc caacaaaagt 1076
tgaagaaaag aaggctccaa aagtatcaga aaacattgga tctgaggatg aatcttctga 1136
agacgagagt gataaagaca gtgaagagcc tca                              1169


<210> 2
<211> 240
<212> PRT
<213> Zea mays

<400> 2
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2

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Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1            5                  10                 15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
            20                  25                 30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
            35                  40                 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
            50                  55                 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65                  70                  75                 80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
                85                  90                 95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
            100                 105                110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp
            115                 120                125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser
            130                 135                140
Arg Arg Pro Arg Gly Arg Arg Val Ala Asp Gly Ala Pro Gly Gly Glu
145                 150                 155                160
Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val
                165                 170                175
Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys
            180                 185                190
Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His
            195                 200                205
Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe
210                 215                 220
Trp Ala Met Met Leu Leu Gln Ser Gln Gln Ala Glu Val Gly Val Gly
225                 230                 235                240
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<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (53)...(736)

<400> 3
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                                                          Met Pro
                                                           1

gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc   106
Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
         5                  10                  15

agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg   154
Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
        20                  25                  30

ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg   202
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
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          35                    40                    45                    50

ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc    250
Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
                55                    60                    65

ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg    298
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
                70                    75                    80

gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag    346
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
            85                    90                    95

gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg    394
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
    100                   105                   110

agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg    442
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly
115                   120                   125                   130

acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc    490
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val
                135                   140                   145

gtc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gct    538
Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala
                150                   155                   160

atg gac acc gtc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc    586
Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser
            165                   170                   175

gct tgc cga cga ggg gat gga ctg cgc gct cgc ggc ggc ggt gta cgg    634
Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly Val Arg
    180                   185                   190

agg aaa agg tgg agt ctt gtc act gct gcg cga gct caa ggc gtg gtt    682
Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly Val Val
195                   200                   205                   210

cga gga gca gcc tct gtt cca ctt cta ctc ggc gtc gat tct tct ggg    730
Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser Ser Gly
                215                   220                   225

cta tga tgctgctgca gtcgcagcag gcggaggtgg gggtggggta acagtgaagc    786
Leu  *


tggtggactt tgcccatgtg gccgagggtg atggggtgat tgaccacaac ttcctgggcg 846
ggctctgcta gctgatcaag ttcgtttctg acattgttcc agagactcct cagacgcagc 906
ctttgggtcc ttcttaa                                                 923

<210> 4
<211> 227
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4

<212> PRT
<213> Zea mays

<400> 4

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Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1               5                  10                  15
Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
            20                  25                  30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
            35                  40                  45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
        50                  55                  60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65                  70                  75                  80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
                85                  90                  95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
           100                 105                 110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp
           115                 120                 125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
        130                 135                 140
Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
145                 150                 155                 160
Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val
                165                 170                 175
Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly
                180                 185                 190
Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly
        195                 200                 205
Val Val Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser
        210                 215                 220
Ser Gly Leu
225
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<210> 5
<211> 923
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (53)...(922)

<400> 5

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accgcttcca ccatcgccac tcgtcacccc ttgctcccat agtccccata cc atg ccc  58
                                                           Met Pro
                                                            1

gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc  106
Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
             5                  10                  15

agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg  154
Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
```

5

```
ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg   202
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
 35                  40                  45                  50

ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc   250
Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
                55                  60                  65

ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg   298
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
                70                  75                  80

gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag   346
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
                85                  90                  95

gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg   394
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
        100                 105                 110

agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg   442
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly
115                 120                 125                 130

acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc   490
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val
                135                 140                 145

ggc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gcc   538
Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala
                150                 155                 160

atg gac acc gcc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc   586
Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser
                165                 170                 175

gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga   634
Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val Tyr Gly
                180                 185                 190

gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc   682
Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe
195                 200                 205                 210

gag gag cag act ctg ttc cac ttc tac tcg gcg tcg att ctt ctg ggc   730
Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly
                215                 220                 225

tat gat gct gct gca gtc gca gca ggc gga ggt ggg ggt ggg gtg acg   778
Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly Val Thr
                230                 235                 240

gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att   826
Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile
```

```
                245                    250                       255
gac cac aac ttc ctg ggc ggg ctc tgc tcg ctg atc aag ttc gtt tct    874
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser
    260             265                 270

gac att gtt cca gag act cct cag acg cag cct ttg ggt cct tct taa    922
Asp Ile Val Pro Glu Thr Pro Gln Thr Gln Pro Leu Gly Pro Ser  *
275             280                 285

g                                                                  923


<210> 6
<211> 289
<212> PRT
<213> Zea mays

<400> 6
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
1               5                   10                  15
Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
            20                  25                  30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
        35                  40                  45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
    50                  55                  60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65                  70                  75                  80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
                85                  90                  95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
            100                 105                 110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp
        115                 120                 125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
    130                 135                 140
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
145                 150                 155                 160
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val
                165                 170                 175
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val
                180                 185                 190
Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala
            195                 200                 205
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu
    210                 215                 220
Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly
225                 230                 235                 240
Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
                245                 250                 255
Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe
            260                 265                 270
Val Ser Asp Ile Val Pro Glu Thr Pro Gln Thr Gln Pro Leu Gly Pro
        275                 280                 285
Ser
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7

<210> 7
<211> 1344
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (52)...(921)

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gcacgaggtc agtccgtcac ccctcgcgcc catagtcccc ttccccatac c atg tcc   57
                                                          Met Ser
                                                           1

gac ctc cac ccg ccg gag cac caa gtc gcc ggc cac cgc gcc tcc gcc   105
Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
            5   10   15

agc aag ctg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg   153
Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
         20   25   30

ctc cag gcc ggc gac cgt ggg gag cac gag gtc gcc ttc tat gag gcg   201
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
 35   40   45   50

ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc   249
Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
                 55   60   65

ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg   297
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
                 70   75   80

gag ccg cat cct cac ctc gtc ctc gac gac ctc ctc gcg ggg ttt cag   345
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Gln
             85   90   95

gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg   393
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
         100   105   110

agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc aag gac cgc ggg   441
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp Arg Gly
115   120   125   130

acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc   489
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val
                 135   140   145

ggc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gcc   537
Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala
             150   155   160

```
atg gac acc gcc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc   585
Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser
        165             170             175

gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga   633
Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val Tyr Gly
        180             185             190

gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc   681
Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe
195             200             205             210

gag gag cag act ctg ttc cac ttc tac tcg gcg tcg att ctt ctg ggc   729
Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly
            215             220             225

tat gat gct gct gca gtc gca gca ggc gga gat ggg ggt ggg gtg acg   777
Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly Val Thr
        230             235             240

gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att   825
Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile
        245             250             255

gac cac aac ttc ctg ggc ggg ctc tgc tcg ctg atc aag ttc gtt tct   873
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser
        260             265             270

gac att gtt ccg gag act cct cat acg cag cct ttg ggt cct tct taa   921
Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro Ser  *
275             280             285

gagaggatcc tggcatttcg atttgataac aaagccctac aagttttgtc tggaaaaaga  981
agcgcctccg agttgtgctg ggtgtggaga tctgagacgg tcgtcggccc acttggttgc 1041
cttgcctttg ccttgcctgc aaacatacgg caacctgctc ctttttttcgc aaccccttac 1101
ttccgaagaa actttttttt tcccactttg ggggttcgat tacgttggat ctggtttgtg 1161
ccactcggtc agaggttgta agcatggagg gaggcgtgtt gatccggcaa ctgtgtcagt 1221
ctttgcgctg cctgccgttt ctgcatggct tttgcctgct gcgatccgat gtgtactgga 1281
gatcgtagtg atggacgtct ctacctccaa acgaatccgt ccgataaaaa aaaaaaaaaa 1341
aaa                                                              1344
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<210> 8
<211> 289
<212> PRT
<213> Zea mays

<400> 8

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Met Ser Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1           5               10              15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
            20              25              30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
            35              40              45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
    50              55              60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
```

9

```
65                      70                      75                      80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
                85                      90                      95
Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
            100                     105                     110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp
        115                     120                     125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
    130                     135                     140
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
145                     150                     155                     160
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val
                165                     170                     175
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val
            180                     185                     190
Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala
        195                     200                    .205
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu
    210                     215                     220
Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly
225                     230                     235                     240
Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
                245                     250                     255
Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe
            260                     265                     270
Val Ser Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro
        275                     280                     285
Ser
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<210> 9
<211> 1105
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (12)...(851)

<400> 9
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gcacgagaaa a atg ctc aag atc ccg gag cac cag gtg gcc ggg cac aag   50
            Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys
             1            5                   10


gcc aag gac gga atc ctg ggc cca ctc gtc gac gat ttt gga aaa ttc   98
Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe
         15              20              25


tac aag ccc ctc cag acc aac aaa gac gac gac acc cgc ggc tcc acc   146
Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr
 30              35              40                      45


gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc gcc cac gac tac tcc   194
Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala Ala His Asp Tyr Ser
             50              55              60
```

10

```
atc cgc tcc ttc ttc ccc gcc ttt cac ggc acc cgc ctc ctg gac gcc   242
Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala
            65              70              75

tcc gac ggc tcc ggt ccc cac cct cac ctg gtc ctg gag gac ctc ctc   290
Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu
            80              85              90

tgc ggc tac tcc aaa ccc tcc gtc atg gac gta aag atc ggc tcc aga   338
Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg
            95              100             105

acc tgg cac ctg gga gac tcc gag gac tac atc tgc aag tgc ctg aag   386
Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys
110             115             120             125

aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tcg gga   434
Lys Asp Arg Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly
            130             135             140

gtc aag gac tct atc tcc tcc tgg gaa cct acc agg aaa tct ctc cag   482
Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln
            145             150             155

tgt cta tcc gcc cat ggt gtt gca ctt gtt ctc aac aag ttc gtt tcc   530
Cys Leu Ser Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser
            160             165             170

tct aat aat atc aac cat gat gat cat cat ccc gat tgc gct ttc gca   578
Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala
            175             180             185

acg gag gtc tac ggc gcc gtt ttg gag cgc ttg cag aag ctc aag gac   626
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp
190             195             200             205

tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt   674
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu
            210             215             220

gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg   722
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu
            225             230             235

gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att   770
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile
            240             245             250

gat cac aac ttc ttg ggt ggc ctt tgt tcc ttc atc aag ttc ctc aag   818
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys
            255             260             265

gat atc cta gca gta gca tgt ctt cac aag tga ctgattttca tcgagttaat 871
Asp Ile Leu Ala Val Ala Cys Leu His Lys  *
270             275
```

11

```
cttattccta tcagaaaata attatgcttg aattagtgtc gcagactaac tgtttgaagt 931
actgtcagaa acaaaataat aatatggact gagaggcaat cttgttctgc taaactccct 991
ttcaagttgc tgtcagatac tagccgtccc ttttcctttt tcatattctg tcaaagtgag 1051
tcatttaata ataataacaa tgtccttcaa ctccaaaaaa aaaaaaaaaa aaaa      1105
```

<210> 10
<211> 279
<212> PRT
<213> Glycine max

<400> 10

```
Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp
1               5                   10                  15
Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro
            20                  25                  30
Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser
            35                  40                  45
Phe Tyr Thr Ser Leu Ala Ala Ala Ala His Asp Tyr Ser Ile Arg Ser
    50                  55                  60
Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly
65                  70                  75                  80
Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr
                85                  90                  95
Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His
            100                 105                 110
Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg
            115                 120                 125
Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp
            130                 135                 140
Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser
145                 150                 155                 160
Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn
                165                 170                 175
Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val
                180                 185                 190
Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu
            195                 200                 205
Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr
            210                 215                 220
Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu
225                 230                 235                 240
Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn
                245                 250                 255
Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys Asp Ile Leu
                260                 265                 270
Ala Val Ala Cys Leu His Lys
                275
```

<210> 11
<211> 1195
<212> DNA
<213> Eucalyptus grandis

<220>

12

<221> CDS
<222> (116)...(1048)

<400> 11
gcaccagctt cttggagtag ttgcccatca gcgtggattt tcattttagt ccatctggct 60
gtgatcaatc gaatctgagt aagtttggag aattttttcg cacatcagat acacc atg 118
                                                                Met
                                                                1

ctc aag gtc ccg gat cat caa gtc gcc ggt cac cgg gga gac ggg gga 166
Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly Gly
          5   10   15

aag ctg ggg cca ctg gtg gat gat tcg ggc cgc ttc tat aag cct ctc 214
Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro Leu
        20   25   30

cag agc gat cat cgc gga gac acg gaa gtg gcc ttt tac gag tca ttc 262
Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser Phe
    35   40   45

tat tcc aat acc gag atc cca ggt cac att cgc aaa ttc ttt cct gcg 310
Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro Ala
50   55   60   65

ttt cac gga act aag act att gag gcg tct gat gga tcg ggt cct caa 358
Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro Gln
                70   75   80

cct cac ctg gtt ctg gag gat ctc gtc tcg ggt cgc acg aac cca tct 406
Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro Ser
            85   90   95

ctc atg gac atc aag act gga tcc aga aca tgg tat ccg gag gcc tct 454
Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala Ser
            100   105   110

gag gag tac atc caa aag tgc tta gag aaa gat cga aat agc aca agc 502
Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr Ser
    115   120   125

gtt tca ttg ggt ttt agg att tct ggg cta agg gta tat caa aat agc 550
Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn Ser
130   135   140   145

gaa gct gga ttt tgg caa cct gag aag aag gtt gtt tat agc ttt aat 598
Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe Asn
                150   155   160

gcg gac ggt gtc agg tcg gct ctg agg aag ttt gtt tct tcc aac ttg 646
Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn Leu
                165   170   175

tct ctg ggt cca aat gtg gat ccg gat tgt ttg tat gca tca aaa gtt 694
Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys Val
            180   185   190

13

```
tac tgt cac cgg ggt gga att ttg gca caa ttg ctt cag ctg aag gaa    742
Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys Glu
    195             200             205

tgg ttt gag gtt cag acg aat tat cac ttc tat tct tgt tca ctc att    790
Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu Ile
210             215             220             225

atc tta tat gac agg gag tct gct ttg gac ggc tgt gca cac ccg aaa    838
Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro Lys
            230             235             240

gtt aaa ctg gtg gac ttt gca cat gtg atg gat ggc cac ggc gtg atc    886
Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val Ile
            245             250             255

gat cac aac ttc ttg ggt ggc ctc tgt tct gta atc aag ttt ata cgt    934
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile Arg
        260             265             270

gac att gct gat gaa gat aac aag tgt gca aag tgc gaa gtc aat ctt    982
Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn Leu
        275             280             285

gga ttg aaa gaa aat ggc ttc tat aag agc agc acg gaa cca gag ctt   1030
Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu Leu
290             295             300             305

gat cac gag gcc tgc tag tggaaactgg agaataactg cattcatgca          1078
Asp His Glu Ala Cys  *
            310

ttcctgcatt cctgctctga caagtggttc agaatgggta taataacagt ctattttagt 1138
caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa     1195


<210> 12
<211> 310
<212> PRT
<213> Eucalyptus grandis

<400> 12
Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly
 1           5               10              15
Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro
            20              25              30
Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser
            35              40              45
Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro
    50              55              60
Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro
65              70              75              80
Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro
            85              90              95
Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala
            100             105             110
```

14

```
Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr
    115                 120                 125
Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn
    130                 135                 140
Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe
145                 150                 155                 160
Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn
                165                 170                 175
Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys
                180                 185                 190
Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys
    195                 200                 205
Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu
    210                 215                 220
Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro
225                 230                 235                 240
Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val
                245                 250                 255
Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile
                260                 265                 270
Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn
    275                 280                 285
Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu
    290                 295                 300
Leu Asp His Glu Ala Cys
305                 310


<210> 13
<211> 1020
<212> DNA
<213> Parthenium argentatum

<220>
<221> CDS
<222> (21)...(908)

<400> 13
gcacgagaac ttcttcagac atg ctc aag gcc cca gat cat cag gtt gct gga    53
                      Met Leu Lys Ala Pro Asp His Gln Val Ala Gly
                       1           5                   10

cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc     101
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly
            15                  20                  25

cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta     149
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val
        30                  35                  40

gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata     197
Ala Phe Tyr Glu Ser Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile
    45                  50                  55

cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc     245
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser
```

15

```
act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct   293
Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala
                80                  85                  90

cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg   341
His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp
                95                  100                 105

gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat   389
Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp
                110                 115                 120

agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa   437
Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln
                125                 130                 135

gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac   485
Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr
140                 145                 150                 155

atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt   533
Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe
                160                 165                 170

gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc   581
Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly
                175                 180                 185

ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata   629
Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile
                190                 195                 200

tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att   677
Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile
                205                 210                 215

tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg   725
Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu
220                 225                 230                 235

gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt   773
Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe
                240                 245                 250

gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt   821
Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly
                255                 260                 265

ggg ctc tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca   869
Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr
                270                 275                 280

aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactctcttc   918
Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu  *
```

16

```
ttgttgcttt tcttcaataa tttatcatga cagtgtttaa ttgtaaagat attcgcttac 978
cggaatatat cttggttatg agtgaaaaaa aaaaaaaaaa aa                     1020
```

<210> 14
<211> 295
<212> PRT
<213> Parthenium argentatum

<400> 14

Met	Leu	Lys	Ala	Pro	Asp	His	Gln	Val	Ala	Gly	His	Glu	Ala	Gly	Leu

Met Leu Lys Ala Pro Asp His Gln Val Ala Gly His Glu Ala Gly Leu
1   5   10   15
Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Arg Phe Tyr Lys Pro
            20   25   30
Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser
        35   40   45
Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro
    50   55   60
Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His
65   70   75   80
Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser
            85   90   95
Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser
            100   105   110
Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser
        115   120   125
Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp
    130   135   140
Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly
145   150   155   160
Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro
            165   170   175
Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu
            180   185   190
Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met
        195   200   205
Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala
    210   215   220
Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala
225   230   235   240
Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp
            245   250   255
Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu
            260   265   270
Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly
    275   280   285
Thr Asn Gly Gln Val Glu Leu
    290   295

<210> 15
<211> 899
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (89)...(424)

<400> 15
gccccaaaat ctctttctcc gctgcgccgc aaacccaccg cttccaccat cgccacccgt 60
caccccttgc tcccatagtc cccatacc atg ccc gac ctc cac ccg ccg gag   112
                                Met Pro Asp Leu His Pro Pro Glu
                                 1   5

cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc   160
His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu
         10   15   20

atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt   208
Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg
 25   30   35   40

ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc   256
Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala
                 45   50   55

gtc ccg gcc cgc atc cga gac acc ttc ttc ccc cgg ttc cac ggc acg   304
Val Pro Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr
             60   65   70

cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc   352
Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu
             75   80   85

gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac   400
Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp
         90   95   100

atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct   454
Ile Lys Ile Gly Ala Ile Thr *
105   110

ccggcgtccg agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc cctgaggtga 514
aggctatgga cattgtcggc gtccgccgcg tgctccggcg ctgcatgtca tccgcttgcc 574
ggcgagggga tggactgcgc gctcgcggcg gcggtgtacg gaggaaaagg tggagtcttg 634
tcacagctgc gcgagctcaa ggcgtggttc gaggggcaga tctgttcca cttctactcg 694
gcgtcgattc ttctgggcta tgatgctgct gcagtcgcag caggcggagg tgggggtggg 754
gtaacagtga agctggtgga ccttgcccat gtggccgagg gtgatggggt gattgaccac 814
aacttcctgg gcgggctctg ctagctgatc aagtttgttt ctgacattgt tccagagact 874
ccttagacgc agcaagggcg aattc   899

<210> 16
<211> 111
<212> PRT
<213> Zea mays

<400> 16
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1   5   10   15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr

18

```
                  20                    25                    30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
          35                    40                    45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
      50                    55                    60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65                    70                    75                    80
Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly
                  85                    90                    95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
                  100                   105                   110
```

<210> 17
<211> 643
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A, T, C or G

<400> 17
```
ggccgtccct gnttttgtta accaccccgc cccaaaatct ctttctccgc tgcgctgcaa 60
acccaccgct tccaccatcg ccactcgtca ccccttgctc ccatagtccc cataccatgc 120
ccgacctcca cccgccggag caccaagtcg ccggtcaccg cgcctccgcc agcaagctgg 180
gcccgctcat cgacggctcc ggcctcttct acaagccgct ccaggccggc gaccgtgggg 240
agcacgaggt cgccttctat gaggcgttct ccgcccacgc cgncgtcccg gcccgcatcc 300
gagacacctt cttcccccgg ttccacggca cgcgactcct ccccaccgag gcgcagcccg 360
gggagccgca tccgcacctc gtcctcgacg acctcctcgc ggggtttgag gcgccctgcg 420
tcgcagacat caagatcggc gccatcacgt ggccaccgag ttcgccggag ccctacatcg 480
ncaagtacct ngccaaggac cgcgggacca cgagcgttct gctcggattc cgcgtcttgc 540
gtccgagtcg tcggccccga gggcgccgtg tggcggacgg agcgccccgg gggtgaangc 600
tatggacacc cgtcggngnc cggcgngtgc ttcgggngct acg                643
```

<210> 18
<211> 519
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)...(519)
<223> n = A, T, C, or G

<400> 18
```
ggtacggang aaaangtgga gtcttgtcac agctgcgcga gctcaangcg tggttcgagg 60
ggcagactct gttccacttc tactcggcgt cgattcttct gggctatgat gctgctgcag 120
tcgcagcagg cggangtggg ggtgggggtaa cagtgaagct ggtggacttt gcccatgtgg 180
ccgagggtga tggggtgatt gaccacaact tcctgggcgg gctctgctan ctgatcaagt 240
ttgtttctga cattgttcca gagactcctc agacgcagcc tttgggtcct tcttaagaaa 300
agatcctggc attttcgatt tgataacaaa ggaancactt tcagctgcca aaaaaaaanc 360
accagtgaag atgaaaataa cattattgag gaaagttccg atnataaccc accanattna 420
aaaaaaaaag gtcccaaatt tccgaaaatn tggatcttaa gaataatctc ctgaaaacan 480
aattataaaa cgtgaaaacc ccggctncnt catttacnc                     519
```

19

<210> 19
<211> 353
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)...(353)
<223> n = A, T, C, or G

<400> 19
ctcaaggcat ggttggagga gcagactctg ttccacttct actcggcgtc gattcttctg 60
ggctatgatg ctgctgcagt cgcancaggc ggaggtgggg gtggggtaac agtgaagctg 120
gtggactttg cccatgtggc cgagggtgat ggggttgatt tgaccacaac ttcctgggcg 180
agctctgcta gctgatcaag ttccgtttct tgacattgtt ccaganactc cttagacgcc 240
agcctttggg tccttcctta aaaaaagatc cctgacnttt ttgatttgat tacnaaggaa 300
acactttcca cttgccnaaa aaaaagccc ntgaggatta aaaaattaac ntt 353

<210> 20
<211> 3416
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (72)...(407)

<400> 20
ccacgcgtcc ggcaaaccca ccgcttccac catcgccacc cgtcacccct tgctcccata 60
gtccccatac c atg ccc gac ctc cac ccg ccg gag cac caa gtc gcc ggt 110
            Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly
            1   5   10

cac cgc gcc tcc gcc agc aag ctg ggc cca ctc atc gac gac tct ggc 158
His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly
    15   20   25

ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag cac gag gtc 206
Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val
    30   35   40   45

gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc 254
Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile
                50   55   60

cga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc ctc ccc acc 302
Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr
                65   70   75

gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc gac gac ctc 350
Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu
        80   85   90

ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag atc ggt gcc 398
Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala

20

```
atc acg tga ccacgagcgt tctgctcgga ttccgcgtct ccggcgtccg          447
Ile Thr  *
110
```

```
agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc ccggaggtga aggctatgga 507
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gctgggtccg tacatgaggt caaggacgcc ttgaagaaca tgttccccag cgagaaagag 1947
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gatgtacatc acttcactaa tcatgaaatc tgtagaaggc gaaactacta gccatatatg 3327
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<210> 21
<211> 111
<212> PRT
<213> Zea mays

<400> 21
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
1   5   10   15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr
            20   25   30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
        35   40   45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
    50   55   60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65   70   75   80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
                85   90   95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
            100   105   110

<210> 22
<211> 1448
<212> DNA
<213> Parthenium argentatum

<220>
<221> CDS
<222> (52)...(1020)

<400> 22
gcacgaggca cactcaatgg ctccgatgct cagaggccaa cggagggtac c atg ctg   57
                                                          Met Leu
                                                           1

cca gct cca gct gtt cct aat ggc acg ggt gct ccg ctt aag gac gaa   105
Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu
          5   10   15

cct tcc aac ccc gat cag gcg cag cac cag cct gac gag cgc gtt caa   153
Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln
        20   25   30

cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt   201
His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys
35   40   45   50

gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat   249
Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp
                55   60   65

gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt   297
Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr Thr Ser
                70   75   80

22

```
gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag    345
Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys
        85                  90                  95

acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa    393
Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys
        100                 105                 110

gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg    441
Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly
115                 120                 125                 130

acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag    489
Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys
                135                 140                 145

atc agc caa ctg gaa cgc atg ata cga aaa ctt cca gga tac aga ttc    537
Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe
        150                 155                 160

tac gcg agt agt ttg ttg atg ctc tat gat cgt ggg gac ggt gag tcg    585
Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser
        165                 170                 175

aag gag aaa gac gca gca ccc tct tta cct aac ggc ttg tcg aac ccg    633
Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser Asn Pro
180                 185                 190

agc aac gaa gac gtt tca aca ata cca tct gga ctt aca tca cca ggg    681
Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly
195                 200                 205                 210

ccg aca gtc gct tct aaa ccg tca ccc aag aag cac gga gag atc aag    729
Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys
                215                 220                 225

ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta    777
Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu
                230                 235                 240

cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga    825
Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg
            245                 250                 255

ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att    873
Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile
        260                 265                 270

tgg aat gac atc aac gag gaa tgg gtc gaa cga ggc gag ggc gag ggc    921
Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly Glu Gly
275                 280                 285                 290

atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg    969
Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val Gly Ala
                295                 300                 305
```

23

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ggc tgg atg gat gat gct ggt ggt gag gat aca ggc tac gcc agt ttc      1017
Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe
        310                     315                 320


taa agaagaggag gaacagcaaa gctgcccacg ctcgacagaa gtcggacagt          1070


cgatattgat acgtccatcc cttttccctt cccttcattt ccacgttcag tctatttcac  1130
attgtgtgca ttttgggttg caagcatggt gttttggtgc ataatggtaa gacaaagggt  1190
aatgaaattg gcaactcttt tggcatgcat cggcgcagca ttttatgggc ggtcagaacc  1250
tctgcgttgt ggcttttagt ttttgaaatt tgcggaatct ggggtgttct tgaggcggat  1310
tctttgtata ttatcataaa gagtagggta gcgctagctc attaatacaa cactttgaat  1370
gtcgtcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  1430
aaaaaaaaaa aaaaaaa                                                 1448


<210> 23
<211> 322
<212> PRT
<213> Parthenium argentatum


<400> 23
Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys
1               5                   10                  15
Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg
            20                  25                  30
Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg
        35                  40                  45
Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu
    50                  55                  60
Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr
65                  70                  75                  80
Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn
                85                  90                  95
Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp
                100                 105                 110
Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp
            115                 120                 125
Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu
    130                 135                 140
Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr
145                 150                 155                 160
Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly
                165                 170                 175
Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser
            180                 185                 190
Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser
        195                 200                 205
Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu
    210                 215                 220
Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp
225                 230                 235                 240
Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile
                245                 250                 255
Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln
                260                 265                 270
```

24

```
Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly
        275                 280                 285
Glu Gly Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val
        290                 295                 300
Gly Ala Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala
305                 310                 315                 320
Ser Phe


<210> 24
<211> 2270
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)...(953)

<400> 24
cc acg cgt ccg cga aaa ttg aga aac att gtt cag tgg acg ccg ttc      47
   Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe
    1               5                  10                  15

ttt caa act tac aaa aaa cag agg tat cca tgg gta cag cta gcc gga     95
Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly
                20                  25                  30

cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag    143
His Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys
            35                  40                  45

aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac    191
Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp
        50                  55                  60

gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac    239
Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp
        65                  70                  75

gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act    287
Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr
 80                  85                  90                  95

tcg ccg tgc gtc atg gac tgc aag atc ggc gtc agg acg tat ctg gaa    335
Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu
                100                 105                 110

gag gaa ctg gcg aaa gcc aaa gag aaa ccc, aag ttg aga aaa gac atg    383
Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met
            115                 120                 125

tac gaa aaa atg att cag ata gac ccc aac gca cca tcg gag gag gaa    431
Tyr Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu
        130                 135                 140
```

```
cac cga ctg aag ggt gtg aca aaa ccg agg tac atg gtt tgg agg gag    479
His Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu
    145             150             155

acg att tcg tcc acg gcc acg ttg ggc ttc cgg atc gag ggg atc aag    527
Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys
160             165             170             175

aaa agc gat gga aaa tcg agc aag gac ttc aag acg aca aag aac cgg    575
Lys Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg
            180             185             190

gac cag gtg atc gaa gcg ttt cga gat ttc gtc gcc ggt ttc ccg cac    623
Asp Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His
            195             200             205

gta atc ccc aag tac ata aac cga ctg aga gcg atc aga gac ata ctg    671
Val Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu
            210             215             220

gtg aac tcc aag ttt ttc act acg cac gag gtg atc ggc agc tcg ctg    719
Val Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu
    225             230             235

ctg ttc gtg cac gac agc aag aac gcc aac ata tgg ctt atc gac ttc    767
Leu Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe
240             245             250             255

gca aag acg ctc ata ctt ccg ccg gac atc cgg atc aac cac acg tcc    815
Ala Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser
            260             265             270

gag tgg gtg gtg ggc aac cac gag gac ggt tac ctg atc ggt atc aac    863
Glu Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn
            275             280             285

aac ctg ctg gac ata ttc acc gat atg aac gcc gcc acc gcg ttt ccc    911
Asn Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro
            290             295             300

gtc acg ctc atc gaa gtc acg gcc ccg tcc gaa gtc acc tga            953
Val Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr  *
            305             310             315

acgccgtcga tccccgccgg taccctgact cgctcggcga cccactcgcc ggtgtcattc 1013
gattccagcc acccactcag tggtcttgcg aatcacgtga cccacccgt  tgacaatgtg 1073
tgataataat aatatgtctg gcgcaaaata ttccaaaaag tcttttttaa attacacttt 1133
cgattttcga cgacaaacaa aatgacgacg tttttccgtac ctacctactg tagggttcgt 1193
tccgattgca atcataattt attttacccc cacccaaccc ccgaaccgtt tatggcccac 1253
cagaggattt gccatcagta ttaaaacaat gatctattat agatgttaaa aaataaatat 1313
tatataatta tacatcatcg cggtgtgttg tgtaaatgc  ctattataat atgtactata 1373
ttatacacat agcatattat aaaaatagta tattattata ttatattata ataatattat 1433
ggttatgtgt gtttgtgtgg aaatccaata atataaaata atagttatta tttttaaata 1493
cttgtacgat aatgggacta ctacgtgtga ttctcaaatg atatatatat attaatattt 1553
taaacgtaca ttttttaattc caaacgtata tgacgtgtgt atatattatt atgatataat 1613
aattactata ctgtgcgtgc gataacataa taattttgta cctaatacat caatcaatta 1673
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26

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tccactgcag tgtcgtgtgg tttttatttc gttgtttat tttatcgcta tcactaaatt 1733
actatttta ttattattat ttttttttt tttcaaaaac tttgttttat aatcagctcc 1793
ctccactacc cttttcacaa cccctcttgt ccatgtatta agcaaataat tatttttta 1853
aatacctatc cacgttacaa cgacaataat aataacaata atagtaccta tactttattt 1913
ttatttcctc acgaaacga gaagtcctca tttctttctc ccgttacagt gtgtgtgtgt 1973
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcgtatgtgt atgtgtgaaa tttttgattt 2033
aattatatat tattataatt ttttctcctt atatttttat ttattattat aacatttttt 2093
ttgtgtgtac agaatattta aataagactt gtaaaagaaa cccttgttat attatttat 2153
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2270
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<210> 25
<211> 316
<212> PRT
<213> Zea mays

<400> 25

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Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe Phe
1               5                   10                  15
Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly His
            20                  25                  30
Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys
        35                  40                  45
Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val
    50                  55                  60
Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp
65                  70                  75                  80
Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser
                85                  90                  95
Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu
                100                 105                 110
Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr
            115                 120                 125
Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His
        130                 135                 140
Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr
145                 150                 155                 160
Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys
                165                 170                 175
Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp
                180                 185                 190
Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val
            195                 200                 205
Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val
    210                 215                 220
Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu Leu
225                 230                 235                 240
Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala
                245                 250                 255
Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu
                260                 265                 270
Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn
                275                 280                 285
Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro Val
    290                 295                 300
Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr
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27

<210> 26
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
accgcttcca ccatcgccac tcgtc   25

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 27
ccttagacgc agcctttggg tccttcttaa   30

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 28
tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa   36

<210> 29
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<400> 29
Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu
 1   5   10   15
Asp Leu Lys Met Gly
            20

<210> 30
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = any amino acid

<400> 30
Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
 1   5   10   15
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
            20   25   30
Gln

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = any amino acid

<400> 31
Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
 1   5   10   15
Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
            20   25   30
Gln

<210> 32
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = any amino acid

<400> 32
Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
 1   5   10   15
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
            20   25   30
Gln

<210> 33
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = any amino acid

<400> 33
Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
1   5   10   15
Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
            20   25   30
Gln

<210> 34
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<221> VARIANT
<222> (1)...(41)
<223> Xaa = any amino acid

<400> 34
Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp
1   5   10   15
Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
            20   25   30
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
        35   40

<210> 35
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
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<223> Xaa = any amino acid

<400> 35
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Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp
1               5                   10              15
Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
            20                  25              30
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
        35              40
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<220>
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<400> 36
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1               5                   10              15
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            20                  25              30
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
        35              40
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<220>
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<221> VARIANT
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<223> Xaa = any amino acid

<400> 37
```
Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp
1               5                   10              15
Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
            20                  25              30
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
        35              40
```